Search time [illegible] Seconds
(without alignments)
[illegible] Million cell updates/sec

Minimum Match [illegible]
Maximum Match [illegible]
Listing first [illegible] summaries

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAS[illegible]	Mycobacterium [illegible]
13	25	100.0	[illegible]	22	AAS[illegible]	Mycobacterium [illegible]
15	25	100.0	209	22	AAS[illegible]	Mycobacterium [illegible]
17	25	100.0	214	22	AAS[illegible]	Mycobacterium [illegible]
19	25	100.0	[illegible]	22	AAS[illegible]	Mycobacterium [illegible]
34	20.2	[illegible]	[illegible]	[illegible]	AAS[illegible]	[illegible]
36	19.2	76.8	[illegible]	22	AAS[illegible]	[illegible]
38	19.2	76.8	[illegible]	[illegible]	AAB[illegible]	[illegible]
43	18.8	[illegible]	[illegible]	[illegible]	AB[illegible]	[illegible]

ALIGNMENTS

RESULT 1
AAS[illegible]
XX
XX
DT 07-SEP-2001 (first entry)
XX
DE Mycobacterium [illegible] fragment.
XX
KW [illegible] fragment; NIM; [illegible]
XX
OS Mycobacterium [illegible]
XX
PN WO[illegible]
XX
PD 03-MAY-2001.
XX
XX
XX
PA (LEUM-) [illegible]
XX
PI Lee H, Park YK, [illegible]
XX
DR WPI; 2001-[illegible]
XX
PT New DNA fragment, [illegible]

```
XX
PS   Claim 1; Page 41; 50pp; English.
XX
CC   The present sequence for Mycobacterium gordonae type IV rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 207 BP; 45 A; 66 C; 66 G; 30 T; 0 other;

  Query Match             100.0%;  Score 25;  DB 22;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAGGAGAAGCGCTACGACCTGGC 25
              |||||||||||||||||||||||||
Db          1 TCAAGGAGAAGCGCTACGACCTGGC 25


RESULT 2
AAS[illegible]
ID   AAS[illegible] standard; DNA; 208 BP.
XX
AC   AAS[illegible];
XX
DT   [illegible] (first entry)
XX
DE   Mycobacterium gordonae type I rpoB gene fragment.
XX
KW   Non tuberculosis mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium gordonae type I.
XX
PN   W[illegible] A1.
XX
PD   [illegible]-MAY-[illegible].
XX
PF   [illegible] 2000WO-KR01223.
XX
PR   [illegible] 99KR-0046795.
XX
PA   (ERUM-) ERUME BIOTECH CO LTD.
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HC;
XX
DR   WPI; [illegible]20/41.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 40; 50pp; English.
XX
CC   The present sequence for Mycobacterium gordonae type I rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA
CC   method. The method comprises obtaining a restriction fragment [illegible]
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; [illegible]
CC   amplifying and digesting the DNA fragment from the microorganism [illegible]
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, [illegible]
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual [illegible]
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS[illegible]) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 4[illegible] A; [illegible] other;

  Query Match             [illegible];  Score 25;  DB 22;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   25;  Conservative    [illegible];  Mismatches    0;  Indels    [illegible]

Qy          1 TCAAGGAGAA[illegible] 25
              [illegible]
Db          1 [illegible] 25


RESULT 3
AAS05202
ID   AAS05202 standard; DNA; [illegible] BP.
XX
AC   AAS05202;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium gordonae type II rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium gordonae type II.
XX
PN   WO2001[illegible] A1.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-KR[illegible].
XX
PR   27-OCT-1999; [illegible]KR-[illegible].
XX
PA   (ERUM-) ERUME BIOTECH [illegible].
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park H[illegible]
XX
DR   WPI; 2001-[illegible]/41.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 40; 50pp; English.
XX
CC   The present sequence for Mycobacterium gordonae type II rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; [illegible]
CC   amplifying and digesting the DNA fragment from the microorganism [illegible]
CC   be identified and comparing the RFLP patterns from the known rpoB gene
```

CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS4227 AAS4212) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence [illegible] BP; [illegible] A; [illegible] others;

Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] AAGAGAAGGTTACATATGGTT [illegible]
[illegible]
Db [illegible] AAGAGAAGGTTACATATGGTT [illegible]

RESULT [illegible]
AAS[illegible]
ID AAS[illegible] standard; DNA; [illegible] BP.
XX
AC AAS[illegible];
XX
DT [illegible] (first entry)
XX
DE Mycobacterium [illegible] type III rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW PCR restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium [illegible] type III.
XX
PN W[illegible]-A.
XX
PD [illegible] MAY [illegible]
XX
PF [illegible] W[illegible] [illegible]
XX
PR [illegible] KR[illegible]
XX
PA ([illegible]M-) [illegible]M[illegible]
XX
PI Lee H, Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
DR W[illegible]
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism.
XX
PS [illegible]
XX
CC The present sequence for Mycobacterium [illegible] type III rpoB gene
CC [illegible]
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 44 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene

CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS[illegible] AAS[illegible]) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence [illegible] BP; [illegible] A; [illegible] others;

Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] AAGAGAAGGTTACATATGGTT [illegible]

Db [illegible] AAGAGAAGGTTACATATGGTT [illegible]

RESULT [illegible]
AAS[illegible]
ID AAS[illegible] standard; DNA; [illegible] BP.
XX
AC AAS[illegible];
XX
DT [illegible] SEP [illegible] (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
KW PCR restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN W[illegible]-A1.
XX
PD [illegible] MAY [illegible]
XX
PF [illegible] 2000; 20[illegible]W-KR[illegible]
XX
PR [illegible] KR[illegible]
XX
PA ([illegible]M-) [illegible]M[illegible]
XX
PI Lee H, Park YK, Bai G, [illegible] Kim Y, Park HJ;
XX
DR W[illegible]
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism.
XX
PS [illegible]
XX
CC The present sequence for Mycobacterium tuberculosis rpoB gene
CC fragment [illegible] rpoB gene fragments (AAS[illegible] AAS[illegible]) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 44 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS[illegible] AAS[illegible]) for
CC detecting specific Mycobacterial species.
XX

SQ Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAGGAGAAGCGCTACGACCTGGC 25
|||||||||||||||||||||||||
Db 1 TCAAGGAGAAGCGCTACGACCTGGC 25

RESULT 6
AAS05206
ID AAS05206 standard; DNA; 208 BP.
XX
AC AAS05206;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mycobacterium terrae rpoB gene fragment.
XX
KW Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW PCR-restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium terrae.
XX
PN WO200131061-A1.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-KR01223.
XX
PR 27-OCT-1999; 99KR-0046795.
XX
PA (BROM-) BROMB BIOTECH CO LTD.
XX
PI Lee H, Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
DR WPI; 2001-365287/31.
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism -
XX
PS Claim 1; Page 42; 50pp; English.
XX
CC The present sequence for Mycobacterium terrae rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAGGAGAAGCGCTACGACCTGGC 25
|||||||||||||||||||||||||
Db 1 TCAAGGAGAAGCGCTACGACCTGGC 25

RESULT 7
AAS05208
ID AAS05208 standard; DNA; 208 BP.
XX
AC AAS05208;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mycobacterium kansasii rpoB gene fragment.
XX
KW Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW PCR-restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium kansasii.
XX
PN WO200131061-A1.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-KR01223.
XX
PR 27-OCT-1999; 99KR-0046795.
XX
PA (BROM-) BROMB BIOTECH CO LTD.
XX
PI Lee H, Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
DR WPI; 2001-365287/31.
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism
XX
PS Claim 1; Page 42; 50pp; English.
XX
CC The present sequence for Mycobacterium kansasii rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence 208 BP; 51 A; 67 C; 57 G; 33 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAGGAGAAGCGCTACGACCTGGC 25
|||||||||||||||||||||||||
Db 1 TCAAGGAGAAGCGCTACGACCTGGC 25

RESULT 8

[illegible] standard; DNA; [illegible]
XX
AA[illegible]
XX
[illegible] (first entry)
XX
[illegible] rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW [illegible] restriction fragment length polymorphism analysis; [illegible]
XX
[illegible]
XX
[illegible] A1.
XX
[illegible]
XX
[illegible] KR [illegible]
XX
[illegible] KR [illegible]
XX
[illegible] BROMB BIOTECH [illegible] LTD.
XX
[illegible] K.H. Y, [illegible]
XX
[illegible]
XX
New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
XX
[illegible] English
XX
The present [illegible] Mycobacterium [illegible] rpoB gene fragment [illegible] 24 rpoB gene fragments (AAS05201 [illegible]) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterial species using a novel PCR restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments, isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or [illegible] epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227 AAS05242) for detecting specific Mycobacterial species.
XX
[illegible] 208 BP; 45 A; [illegible] 28 [illegible] other;

Query Match [illegible] Score 25; DB 22; Length 208;
Best Local Similarity [illegible] Pred. No. [illegible]
Matches [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible] AAGAGAA[illegible]A[illegible]
[illegible] AAGAGAA[illegible]A[illegible]

[illegible]
XX
AA[illegible] standard; DNA; [illegible]
XX
AA[illegible]
XX
[illegible] (first entry)
XX
DE Mycobacterium [illegible] rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
KW PCR restriction fragment length polymorphism analysis; [illegible]
XX
OS Mycobacterium [illegible]
XX
PN WO200[illegible] A1.
XX
PD [illegible] MAY [illegible]
XX
PF [illegible] KR [illegible]
XX
PR [illegible] KR [illegible]
XX
PA (BROM-) BROMB BIOTECH [illegible] LTD.
XX
PI [illegible] K.H. Y, [illegible]
XX
DR WPI; [illegible]
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism
XX
PS Claim [illegible] English.
XX
CC The present [illegible] Mycobacterium [illegible] rpoB gene
CC fragment [illegible] 24 rpoB gene fragments (AAS05201 [illegible]) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterial species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments, isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or [illegible] epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS05227 AAS05242) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence 20[illegible] BP; [illegible] other;

Query Match [illegible] Length [illegible]
Best Local Similarity [illegible]
Matches [illegible] Mismatches [illegible] Gaps [illegible]

Qy [illegible] AAGAGAA[illegible]A[illegible]
Db [illegible] AAGAGAA[illegible]A[illegible]

RESULT [illegible]
AAS0[illegible]
ID AAS0[illegible] standard; DNA; [illegible]
XX
AC AAS0[illegible]
XX
DT [illegible]
XX
DE Mycobacterium [illegible] rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
KW PCR restriction fragment length polymorphism analysis; [illegible]
XX

```
OS   Mycobacterium avium.
XX
PN   WO[illegible] A1.
XX
PD   [illegible] MAY [illegible].
XX
PF   27 [illegible] 2000WO-KR01223.
XX
PR   27 [illegible]-1999;   99KR-0046795.
XX
PA   (EPUM ) EPUME BI-TECH CO LTD.
XX
PI   Lee H, Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
DR   WPI; 2001-[illegible]520/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism -
XX
PS   Claim 1; Page 44; 50pp; English.
XX
CC   The present sequence for Mycobacterium avium rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence [illegible] BP; 44 A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             100.0%;  Score 25;  DB 22;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 25
              |||||||||||||||||||||||||
Db          1 [illegible] 25


RESULT [illegible]
AAS[illegible]
ID   AAS[illegible] standard; DNA; 208 BP.
XX
AC   AAS[illegible];
XX
DT   [illegible] 2001  (first entry)
XX
DE   Mycobacterium bovis rpoB gene fragment.
XX
KW   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium bovis.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible] MAY [illegible].
XX
PF   27-OCT-2000; 2000WO-KR01223.
XX
PR   27-OCT-1999;   99KR-[illegible].
XX
PA   (EPUM ) EPUME BI-TECH [illegible].
XX
PI   Lee H, Park YK, Bai [illegible], Kim S, Cho S, Kim Y, Park HJ;
XX
DR   WPI; 2001-[illegible]520/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 45; 50pp; English.
XX
CC   The present sequence for Mycobacterium bovis rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 46 A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             100.0%;  Score 25;  DB 22;  Length 208;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   25;  Conservative    [illegible];  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy          1 [illegible]
              [illegible]
Db          1 TCAAGGAGAAGC[illegible]TACGAC[illegible]


RESULT 12
AAS05[illegible]
ID   AAS05[illegible] standard; DNA; [illegible] BP.
XX
AC   AAS05[illegible];
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium [illegible] rpoB gene fragment.
XX
KW   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium [illegible].
XX
PN   WO200130[illegible] A1.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-KR01223.
XX
PR   27-OCT-1999;   99KR-0046795.
XX
PA   (EPUM ) EPUME BI-TECH [illegible].
XX
```

```
PA   [illegible] Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
PT   [illegible]
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   [illegible] and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 1?; [illegible] English.
XX
CC   The present sequence is a Mycobacterium [illegible] rpoB gene
CC   fragment [illegible] of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy          [illegible] TCAAAGAGAAACTCTACAACATTCCC [illegible]

Db          [illegible] TCAAAGAGAAACTTCATCAACATTCCC [illegible]


RESULT [illegible]
AAS0[illegible]
ID   AAS0[illegible] standard; DNA; [illegible] BP.
XX
AC   AAS0[illegible];
XX
DT   [illegible] (first entry)
XX
DE   M. [illegible] rpoB gene fragment.
XX
KW   [illegible] mycobacterial rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR restriction fragment length polymorphism analysis; [illegible]
XX
OS   Mycobacterium [illegible]
XX
PN   WO200[illegible]-A1.
XX
PD   [illegible] MAY [illegible]
XX
PF   [illegible] WO-KR[illegible]
XX
PR   [illegible]
XX
PA   [illegible] ) [illegible]
XX
PI   [illegible] Park YK, [illegible] Cho S, Kim Y, Park [illegible]
XX
DR   WPI; [illegible]
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   [illegible] and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 4?; Suppl. English.
XX
CC   The present sequence is a Mycobacterium [illegible] rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments [illegible]
CC   in the diagnosis and identification of Mycobacterium species [illegible]
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, [illegible]
CC   diagnosis or to obtain epidemiological and pathogenesis [illegible]
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in [illegible]
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual [illegible]
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) [illegible]
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 40 A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy          [illegible] TCAAAGAGAAACTTCATCAACATTCCC [illegible]

Db          [illegible] TCAAAGAGAAACTTCATCAACATTCCC [illegible]


RESULT 14
AAS0[illegible]
ID   AAS0[illegible] standard; DNA; [illegible] BP.
XX
AC   AAS0[illegible];
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium haemophilum rpoB gene fragment.
XX
KW   Non tuberculous mycobacterial rpoB gene fragment; NTM; HIV; PRA; [illegible]
KW   PCR restriction fragment length polymorphism analysis; [illegible]
XX
OS   Mycobacterium haemophilum.
XX
PN   WO200[illegible]-A1.
XX
PD   [illegible] MAY 2001.
XX
PF   [illegible] WO-KR[illegible]
XX
PR   [illegible]
XX
PA   (KREM-) [illegible]
XX
PI   [illegible] Park YK, [illegible] Cho S, Kim Y, Park [illegible]
XX
DR   WPI; [illegible]
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   [illegible] and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page [illegible]; [illegible]
XX
CC   The present sequence is a Mycobacterium haemophilum rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) [illegible]
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```
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 45 A; 57 C; 70 G; 36 T; 0 other;

  Query Match             100.0%;  Score 25;  DB 22;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAGGAGAAGCGCTACGACCTGGC 25
              |||||||||||||||||||||||||
Db          1 TCAAGGAGAAGCGCTACGACCTGGC 25


RESULT [illegible]
AAS[illegible]
ID   AAS[illegible] standard; DNA; 208 BP.
XX
AC   AAS[illegible];
XX
DT   [illegible]-SEP-2002  (first entry)
XX
DE   Mycobacterium xenopi rpoB gene fragment.
XX
KW   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR-restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium xenopi.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible]-MAY-[illegible].
XX
PF   [illegible]  2000WO-KR01223.
XX
PR   [illegible] 1999;  99KR-0046795.
XX
PA   (BREM-) BRUME BIOTECH CO LTD.
XX
PI   [illegible]  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HJ;
XX
DR   WPI; [illegible]/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism -
XX
PS   Claim [illegible]; Page 47; 50pp; English.
XX
CC   The present sequence for Mycobacterium xenopi rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 51 A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score 25;  DB 22;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAGGAGAAG[illegible]TACGAC[illegible] 25
              |||||||||||||||||||||||||
Db          1 TCAAGGAGAAG[illegible]TACGAC[illegible] 25


Search completed: [illegible]
Job time : [illegible] secs
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[illegible] nucleic search, using sw model

Run on: July 24, 2003, 22:00:20 ; Search time 85.2128 Seconds
(without alignments)
528.559 Million cell updates/sec

Title: US-10-058-422-3
[illegible]
[illegible]

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: [illegible] seqs, [illegible] residues

Total number of hits satisfying chosen parameters: [illegible]

Minimum DB seq length: [illegible]
Maximum DB seq length: [illegible]

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_[illegible]:*
[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
[illegible]	[illegible]	[illegible]	20	22	AAS05227	Mycobacterium spec
[illegible]	[illegible]	[illegible]	20	22	AAS05226	Mycobacterium intr
[illegible]	[illegible]	[illegible]	20	22	AAS05204	Mycobacterium gord
[illegible]	[illegible]	[illegible]	208	22	AAS05203	Mycobacterium gord
[illegible]	[illegible]	[illegible]	208	22	AAS05205	Mycobacterium gord
[illegible]	[illegible]	[illegible]	208	22	AAS05208	Mycobacterium kans
[illegible]	[illegible]	[illegible]	208	22	AAS05210	Mycobacterium ulce
[illegible]	[illegible]	[illegible]	208	22	AAS05211	Mycobacterium mari
[illegible]	[illegible]	[illegible]	208	22	AAS05219	Mycobacterium aviu
10	20	100.0	[illegible]	[illegible]	[illegible]	[illegible]
11	20	100.0	[illegible]	22	[illegible]	[illegible]
12	20	100.0	[illegible]	22	[illegible]	[illegible]
13	20	100.0	[illegible]	22	[illegible]	[illegible]
14	20	100.0	[illegible]	22	[illegible]	[illegible]
15	20	100.0	234	22	[illegible]	[illegible]
16	20	100.0	[illegible]	22	[illegible]	[illegible]
17	19	95.0	234	22	[illegible]	[illegible]
18	18.4	92.0	[illegible]	22	[illegible]	[illegible]
19	18.4	92.0	[illegible]	[illegible]	[illegible]	[illegible]
20	18.4	92.0	[illegible]	22	[illegible]	[illegible]
21	18.4	92.0	[illegible]	22	[illegible]	[illegible]
22	18.4	92.0	[illegible]	[illegible]	[illegible]	[illegible]
23	18.4	92.0	[illegible]	[illegible]	[illegible]	[illegible]
24	18.4	92.0	211	22	AAS05214	[illegible]
25	18.4	92.0	[illegible]	22	[illegible]	[illegible]
26	18.4	92.0	[illegible]	17	[illegible]	[illegible]
27	18.4	92.0	[illegible]	22	[illegible]	[illegible]
28	18.4	92.0	[illegible]	22	[illegible]	[illegible]
29	18.4	92.0	[illegible]	21	[illegible]	[illegible]
30	18.4	92.0	[illegible]	21	[illegible]	[illegible]
31	18.4	92.0	44[illegible]	22	[illegible]	[illegible]
32	18.4	92.0	441[illegible]	22	[illegible]	[illegible]
33	16.8	84.0	[illegible]	[illegible]	[illegible]	[illegible]
34	16.8	84.0	[illegible]	[illegible]	[illegible]	[illegible]
35	16.8	84.0	[illegible]	11	[illegible]	[illegible]
36	16.8	84.0	[illegible]	[illegible]	[illegible]	[illegible]
37	16.8	84.0	[illegible]	22	[illegible]	[illegible]
c 38	16.8	84.0	[illegible]	22	[illegible]	[illegible]
c 39	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
c 40	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
c 41	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
c 42	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
c 43	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
44	16.4	82.0	[illegible]	[illegible]	[illegible]	[illegible]
c 45	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

ALIGNMENTS

RESULT 1
AAS05227
ID AAS05227 standard; DNA; [illegible]
XX
AC AAS05227;
XX
DT 07-SEP-2001 (first entry)
XX
DE [illegible] AN MYC.
XX
KW [illegible]
KW [illegible] restriction fragment length polymorphism analysis; [illegible]
XX
OS Mycobacterium sp.
XX
PN WO200131061-A1.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-KR-[illegible]
XX
PR 27-OCT-1999; 99KR-[illegible]
XX
PA (BRUM-) BRUME BIOTECH [illegible]
XX
PI Lee H, Park YK, [illegible] Kim Y, Park [illegible]
XX
DR WPI; 2001-[illegible]
XX
PT New DNA fragments from the [illegible]
PT diagnosis and identification [illegible] mycobacterial species [illegible]
PT restriction fragment length polymorphism

```
XX
PS   Claim 1; Page 15; 50pp; English.
XX
CC   The present sequence for Mycobacterium species oligonucleotide
CC   probe PAN MYC can be used to detect all mycobacterial species. It is
CC   1 of 16 oligonucleotide probes (AAS05227-AAS05242) that can be used to
CC   detect specific mycobacterial species. The probes are described in an
CC   invention relating to the use of rpoB gene fragments (AAS05201-AAS05224)
CC   from various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests.
XX
SQ   Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACGTCGTCGCCACCATCGA 20
              ||||||||||||||||||||
Db          1 GACGTCGTCGCCACCATCGA 20

RESULT 2
AAS05220
ID   AAS05220 standard; DNA; 205 BP.
XX
AC   AAS05220;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium intracellulare rpoB gene fragment.
XX
KW   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR-restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium intracellulare.
XX
PN   WO200131061-A1.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-KR01223.
XX
PR   27-OCT-1999;   99KR-0046795.
XX
PA   (BROM ) BROMB BIOTECH CO LTD.
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HJ;
XX
DR   WPI; 2001-300520/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism -
XX
PS   Claim 1; Page 46; 50pp; English.
XX
CC   The present sequence for Mycobacterium intracellulare rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 205 BP; 44 A; 69 C; 67 G; 25 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 205;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACGTCGTCGCCACCATCGA 20
              ||||||||||||||||||||
Db        108 GACGTCGTCGCCACCATCGA 127

RESULT 3
AAS05204
ID   AAS05204 standard; DNA; 207 BP.
XX
AC   AAS05204;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium gordonae type IV rpoB gene fragment.
XX
KW   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR-restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium gordonae type IV.
XX
PN   WO200131061-A1.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-KR01223.
XX
PR   27-OCT-1999;   99KR-0046795.
XX
PA   (BROM ) BROMB BIOTECH CO LTD.
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HJ;
XX
DR   WPI; 2001-300520/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 41; 50pp; English.
XX
CC   The present sequence for Mycobacterium gordonae type IV rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
```

CC [illegible] and [illegible] the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis, to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non tuberculous mycobacteria (NTM) encountered in patients infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS[illegible] AAS[illegible]) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence [illegible] BP; [illegible] A; [illegible] others;

Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible] [illegible] GATCTTCTTTATTAT[illegible]A [illegible]

[illegible] [illegible] GATCTTCTT[illegible]ATTAT[illegible]A [illegible]

RESULT [illegible]
AAS[illegible]
ID AAS[illegible] standard; DNA; [illegible] BP.
XX
AC [illegible]
XX
DT [illegible] (first entry)
XX
DE Mycobacterium [illegible] type [illegible] rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW PCR restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium [illegible] type [illegible]
XX
PN W[illegible]A1.
XX
PD [illegible] MAY [illegible]
XX
PF [illegible] 2000; 2000W[illegible]
XX
PR [illegible]
XX
PA (BRUM-) BRUME BIOTECH [illegible]
XX
PI [illegible] Park [illegible] Kim Y, Park H.
XX
DR WPI; [illegible]/[illegible].
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism.
XX
PS [illegible]
XX
CC The present sequence is a Mycobacterium [illegible] type [illegible] rpoB gene
CC fragment [illegible] rpoB gene fragments (AAS[illegible]-AAS[illegible]) from
CC various Mycobacterium species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the [illegible] rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis, to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae

CC and non tuberculous mycobacteria (NTM) encountered in patients infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS[illegible] AAS[illegible]) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence [illegible] BP; [illegible] A; [illegible] others;

Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] GATCTTCTT[illegible]ATTAT[illegible]A [illegible]

Db [illegible] GATCTTCTT[illegible]A [illegible]

RESULT [illegible]
AAS[illegible]
ID AAS[illegible] standard; DNA; [illegible] BP.
XX
AC AAS[illegible];
XX
DT [illegible] SEP 2001 (first entry)
XX
DE Mycobacterium [illegible] type [illegible] rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
KW PCR restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium [illegible] type [illegible]
XX
PN WO2001[illegible]-A1.
XX
PD [illegible] MAY [illegible]
XX
PF [illegible] 2000; 2000WO-[illegible]
XX
PR [illegible] KR-[illegible]
XX
PA (BRUM-) BRUME BIOTECH [illegible]
XX
PI [illegible] Park YK, [illegible] Kim Y, Park H.
XX
DR WPI; 2001-[illegible]/[illegible].
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism.
XX
PS [illegible]
XX
CC The present sequence is a Mycobacterium [illegible] type [illegible] rpoB gene
CC fragment [illegible] rpoB gene fragments (AAS[illegible] AAS[illegible]) from
CC various Mycobacterium species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the [illegible] rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis, to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non tuberculous mycobacteria (NTM) encountered in patients infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS[illegible] AAS[illegible]) for

```
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 46 A; 69 C; 63 G; 30 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACGTCGTCGCCACCATCGA 20
              ||||||||||||||||||||
Db        108 GACGTCGTCGCCACCATCGA 127


RESULT 6
AAS[illegible]
ID   AAS[illegible] standard; DNA; 208 BP.
XX
AC   AAS[illegible];
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium kansasii rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria, rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium kansasii.
XX
PN   W[illegible] A1.
XX
PD   [illegible]-MAY-2001.
XX
PF   [illegible]-2000; 2000WO-KR01223.
XX
PR   27-OCT-1999;   99KR-0046795.
XX
PA   (ERUM-) ERUME BI[illegible]TECH CO LTD.
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HJ;
XX
DR   WPI; 2001-[illegible]0520/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 42; 50pp; English.
XX
CC   The present sequence for Mycobacterium kansasii rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05.12) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; 51 A; 65 C; 65 G; 27 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACGTCGTCGCCACCATCGA 20
              ||||||||||||||||||||
Db        108 GACGTCGTCGCCACCATCGA 127


RESULT 7
AAS05210
ID   AAS05210 standard; DNA; 208 BP.
XX
AC   AAS05210;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mycobacterium ulcerans rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR-restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium ulcerans.
XX
PN   WO200131061 A1.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-KR[illegible].
XX
PR   27-OCT-1999;   99KR-[illegible].
XX
PA   (ERUM-) ERUME BI[illegible]TECH CO LTD.
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HJ;
XX
DR   WPI; 2001-[illegible]20/31.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 43; 50pp; English.
XX
CC   The present sequence for Mycobacterium ulcerans rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05[illegible]) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 208 BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score [illegible];  DB 22;  Length 2[illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    [illegible];

Qy          1 GACGTCGTCGCCACCATCGA 20
              ||||||||||||||||||||
Db        108 GACGTCGTCGCCACCATCGA 127
```

```
[illegible]
ID   AA[illegible] standard; DNA; [illegible]
XX
AC   AA[illegible]
XX
DT   [illegible] (first entry)
XX
DE   Mycobacterium marinum rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; PCR;
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium marinum.
XX
PN   WO[illegible] A1.
XX
PD   [illegible] MAY [illegible]
XX
PF   [illegible]
XX
PR   [illegible]
XX
PA   (BROM-) BROMB [illegible]
XX
PI   [illegible] YK, Bai [illegible], Kim S, [illegible] S, Kim Y, Park HJ;
XX
DR   WPI; [illegible]
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 44; [illegible] English.
XX
CC   The present sequence for Mycobacterium marinum rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS0[illegible] AAS0[illegible]224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS[illegible] AAS0[illegible]242) for
CC   detecting specific Mycobacterial species
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] other;

  Query Match [illegible]
  Best Local Similarity [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy  [illegible] GATT[illegible]TAT[illegible]A [illegible]
                [illegible]
Db  [illegible] GATT[illegible]TAT[illegible]A [illegible]


RESULT [illegible]
AAS[illegible]
ID   AA[illegible] standard; DNA; [illegible]
XX
AC   AA[illegible]
XX
DT   [illegible] SEP [illegible] (first entry)
XX
DE   Mycobacterium [illegible] rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
KW   PCR restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium [illegible]
XX
PN   WO2001[illegible] A1.
XX
PD   03 MAY [illegible]
XX
PF   27-OCT-[illegible] [illegible] KR[illegible]
XX
PR   27-OCT-[illegible] KR[illegible]
XX
PA   (BROM-) BROMB [illegible]
XX
PI   Lee H, [illegible] YK, Bai [illegible], Kim [illegible], [illegible], Kim Y, Park HJ;
XX
DR   WPI; 2001-[illegible]
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim 1; Page 44; [illegible] English.
XX
CC   The present sequence for Mycobacterium [illegible] rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS0[illegible] AAS[illegible]) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual [illegible]
CC   tests. Also described are oligonucleotide probes (AAS[illegible] AAS[illegible]) for
CC   detecting specific Mycobacterial species
XX
SQ   Sequence [illegible] BP; 44 A; [illegible] other;

  Query Match [illegible]
  Best Local Similarity [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy  [illegible] GATT[illegible]TAT[illegible]A [illegible]
                [illegible]
Db  [illegible] GATT[illegible]TAT[illegible]A [illegible]


RESULT [illegible]
AAS[illegible]
ID   AAS[illegible] standard; DNA; [illegible]
XX
AC   AAS0[illegible]
XX
DT   07-SEP-2001 (first entry)
XX
DE   Mycobacterium [illegible] rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; [illegible]
```

KW PCR-restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium celatum.
XX
PN W[illegible] A1.
XX
PD [illegible] MAY 2001.
XX
PF 27-OCT-2000; 2000WO-KR01223.
XX
PR 27-OCT-1999; 99KR-0046795.
XX
PA (KRUM-) KRUME BIOTECH CO LTD.
XX
PI Lee H, Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
DR WPI; 2001-[illegible]20/31.
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism -
XX
PS Claim 1; Page 45; 50pp; English.
XX
CC The present sequence for Mycobacterium celatum rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS05227-AAS05212) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence 208 BP; 48 A; 71 C; 64 G; 25 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGTCGCCACCATCGA 20
||||||||||||||||||||
Db 108 CAAGTCGTCGCCACCATCGA 127

RESULT 11
AAS05224
ID AAS05224 standard; DNA; 208 BP.
XX
AC AAS05224;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mycobacterium fortuitum rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW PCR-restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium fortuitum.
XX
PN W[illegible] A1.
XX
PD [illegible] MAY 2001.
XX
PF 27-OCT-2000; 2000WO-KR01223.
XX
PR 27-OCT-1999; 99KR-0046795.
XX
PA (KRUM-) KRUME BIOTECH CO LTD.
XX
PI Lee H, Park YK, Bai G, Kim S, Cho S, Kim Y, Park HJ;
XX
DR WPI; 2001-[illegible]20/31.
XX
PT New DNA fragments from the rpoB gene of mycobacteria, useful for
PT diagnosis and identification of many mycobacterial species by
PT restriction fragment length polymorphism -
XX
PS Claim 1; Page 46; 50pp; English.
XX
CC The present sequence for Mycobacterium fortuitum rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AAS05227-AAS05212) for
CC detecting specific Mycobacterial species.
XX
SQ Sequence 208 BP; 4[illegible] A; [illegible] C; [illegible] G; 27 T; [illegible] other;

Query Match [illegible]; Score [illegible]; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 [illegible] 20
[illegible]
Db 108 [illegible] 127

RESULT 12
AAS05223
ID AAS05223 standard; DNA; 208 BP.
XX
AC AAS05223;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mycobacterium haemophilum rpoB gene fragment.
XX
KW Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW PCR-restriction fragment length polymorphism analysis; ds.
XX
OS Mycobacterium haemophilum.
XX
PN WO200131[illegible] A1.
XX
PD [illegible] MAY 2001.
XX
PF 27-OCT-2000; 2000WO-KR01223.
XX
PR 27-OCT-1999; 99KR-0046795.
XX

```
[illegible]
XX
PI   [illegible] Park YK, [illegible] Kim [illegible] Kim [illegible] Park HJ;
XX
DR   WPI; [illegible]
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism
XX
PS   Claim [illegible]; Page 47; [illegible]pp; English.
XX
CC   The present sequence for Mycobacterium haemophilum rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS[illegible]201-AAS[illegible]224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS[illegible]227 AAS[illegible]212) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] other;

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy   [illegible] GATTTTTTTAATATTGA 20
            [illegible]
Db   [illegible] GATTTTTTTAATATTGA 127


RESULT [illegible]
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ID   AAS[illegible] standard; DNA; [illegible] BP.
XX
AC   AAS[illegible]
XX
DT   [illegible] (first entry)
XX
DE   Mycobacterium [illegible] rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR restriction fragment length polymorphism analysis; [illegible]
XX
OS   Mycobacterium [illegible]
XX
PN   W[illegible]
XX
PD   [illegible] MAY [illegible]
XX
PF   [illegible] 2001 [illegible] KR [illegible]
XX
PR   [illegible] KR [illegible]
XX
PA   ([illegible]) [illegible]
XX
PI   [illegible] Park YK, [illegible] Kim [illegible] Kim [illegible] Park HJ;
XX
DR   WPI; [illegible]/41.
XX
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```
PT   New DNA fragments [illegible] mycobacteria, useful for
PT   diagnosis and identification [illegible] mycobacterial species by
PT   restriction fragment length [illegible]
XX
PS   Claim [illegible]; Page 47; [illegible]pp; English.
XX
CC   The present sequence for M[illegible] rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS[illegible]-AAS[illegible]) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS[illegible]-AAS[illegible]) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] other;

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy   [illegible] GATTTTTTTAATATTGA [illegible]
            [illegible]
Db   [illegible] GATTTTTTTAATATTGA [illegible]


RESULT 14
AAS[illegible]214
ID   AAS[illegible] standard; DNA; [illegible]
XX
AC   AAS[illegible]
XX
DT   [illegible] (first entry)
XX
DE   Mycobacterium [illegible] rpoB gene fragment.
XX
KW   Non tuberculous mycobacteria; rpoB gene fragment; NTM; HIV;
KW   PCR restriction fragment length polymorphism analysis; [illegible]
XX
OS   Mycobacterium [illegible]
XX
PN   W[illegible]
XX
PD   [illegible] MAY [illegible]
XX
PF   [illegible] 2001 [illegible] KR [illegible]
XX
PR   [illegible] KR [illegible]
XX
PA   ([illegible]) [illegible]
XX
PI   [illegible] Park YK, [illegible] Kim [illegible] Kim [illegible] Park HJ;
XX
DR   WPI; [illegible]
XX
PT   New DNA fragments [illegible] mycobacteria, useful for
PT   diagnosis and identification [illegible] mycobacterial species by
PT   restriction fragment length [illegible]
XX
PS   Claim [illegible]; Page [illegible]; [illegible]pp; English.
XX
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```
CC   The present sequence for Mycobacterium flavescens rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC   amplifying and digesting the DNA fragment from the microorganism to
CC   be identified and comparing the RFLP patterns from the known rpoB gene
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species, e.g. for
CC   diagnosis or to obtain epidemiological and pathogenesis information for
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual biochemical
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 211 BP; 49 A; 65 C; 70 G; 27 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 211;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCGTGGCCACCATCGA 20
                [illegible]
Db        111 GATCGTGGCCACCATCGA 130


RESULT [illegible]
AAS05222
ID   AAS05222 standard; DNA; 214 BP.
XX
AC   AAS05222;
XX
DT   [illegible] SEP 2001  (first entry)
XX
DE   Mycobacterium abscessus rpoB gene fragment.
XX
KW   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
KW   PCR-restriction fragment length polymorphism analysis; ds.
XX
OS   Mycobacterium abscessus.
XX
PN   WO200134061-A1.
XX
PD   [illegible] MAY 2001.
XX
PF   [illegible] 2000WO-KR01223.
XX
PR   [illegible]   99KR-0046795.
XX
PA   (BRUM-) BRUME BIOTECH CO LTD.
XX
PI   Lee H,  Park YK,  Bai G,  Kim S,  Cho S,  Kim Y,  Park HI;
XX
DR   WPI; [illegible]/41.
XX
PT   New DNA fragments from the rpoB gene of mycobacteria, useful for
PT   diagnosis and identification of many mycobacterial species by
PT   restriction fragment length polymorphism -
XX
PS   Claim [illegible]; Page 40; 58pp; English.
XX
CC   The present sequence for Mycobacterium abscessus rpoB gene
CC   fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC   various Mycobacterial species. These rpoB gene fragments can be used
CC   in the diagnosis and identification of Mycobacterium species using a
CC   novel PCR-restriction fragment length polymorphism analysis (PRA)
CC   method. The method comprises obtaining a restriction fragment length
CC   polymorphism (RFLP) pattern of the 24 rpoB gene fragments; [illegible]
CC   amplifying and digesting the DNA fragment from the micro[illegible]
CC   be identified and comparing the RFLP patterns from the known [illegible]
CC   fragments with the unidentified fragment. The rpoB gene fragments
CC   are useful to identify a wide range of Mycobacterium species [illegible]
CC   diagnosis or to obtain epidemiological and pathogenesis information [illegible]
CC   selection of appropriate therapies, including M. tuberculosis, M. leprae
CC   and non tuberculous mycobacteria (NTM) encountered in subjects infected
CC   with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC   fragments is rapid, precise, simple and cost effective (only 1 PCR
CC   required), and can differentiate between many species in a single
CC   experiment, including those difficult to distinguish by usual [illegible]
CC   tests. Also described are oligonucleotide probes (AAS05227-AAS[illegible]) for
CC   detecting specific Mycobacterial species.
XX
SQ   Sequence 214 BP; 4[illegible] A; [illegible] C; 72 G; 2[illegible] T; 0 other;

  Query Match             [illegible];  Score 2[illegible];  DB 22;  Length 214;
  Best Local Similarity   [illegible];  Pred. No. 1[illegible];
  Matches   20;  Conservative    [illegible];  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy          1 [illegible]
              [illegible]
Db        114 [illegible]


Search completed: July [illegible]
Job time : [illegible]1.2128 secs
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Search time [illegible] Seconds
(without alignments)
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Minimum Match [illegible]
Maximum Match 100%
Listing first 45 summaries

[illegible]

SUMMARIES

[illegible]

ALIGNMENTS

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DEFINITION [illegible]
ACCESSION [illegible]
VERSION [illegible]
KEYWORDS
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
[illegible]
REFERENCE [illegible]
AUTHORS [illegible]

```
            [illegible],M.R., Fattorini,L. and Orefici,G.
  TITLE     rpoB mutations in multidrug resistant strains of Mycobacterium
            tuberculosis isolated in Italy
  JOURNAL   J. Clin. Microbiol. 37 (4), 1197-1199 (1999)
  MEDLINE   [illegible]
   PUBMED   10074552
REFERENCE   2  (bases 1 to 278)
  AUTHORS   Orru,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-1998) Dip. Biologia Molecolare, Sezione di
            Microbiologia, Universita' di Siena, Via Laterina 8, Siena 53100,
            Italy
FEATURES             Location/Qualifiers
     source          1..278
                     /organism="Mycobacterium tuberculosis"
                     /isolate="Rm19"
                     /db_xref="taxon:1773"
                     /note="rifampicin-resistant"
     gene            <1..>278
                     /gene="rpoB"
     CDS             <1..>278
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /product="rifampicin-resistant RNA polymerase
                     beta-subunit"
                     /protein_id="AAC12776.1"
                     /db_xref="GI:3025882"
                     /translation="[illegible]
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BASE COUNT       46 a     92 c     91 g     49 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        [illegible] ACGGGTGCACGTCGCGGACCTCCA 158

RESULT [illegible]
AF[illegible]
LOCUS       AF055893               278 bp    DNA     linear   BCT [illegible]
DEFINITION  Mycobacterium tuberculosis isolate F7 rifampicin resistant RNA
            polymerase beta-subunit (rpoB) gene, partial cds.
ACCESSION   AF055893
VERSION     AF055893.1  GI:3025885
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 278)
  AUTHORS   [illegible],G., Meloni,M., Tona,E., Orru,G., Theresen,[illegible], Rios,M.[illegible],
            [illegible],M.R., Fattorini,L. and Orefici,G.
  TITLE     rpoB mutations in multidrug resistant strains of Mycobacterium
            tuberculosis isolated in Italy
  JOURNAL   J. Clin. Microbiol. 37 (4), 1197-1199 (1999)
  MEDLINE   [illegible]
   PUBMED   10074552
REFERENCE   2  (bases 1 to 278)
  AUTHORS   Orru,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-1998) Dip. Biologia Molecolare, Sezione di
            Microbiologia, Universita' di Siena, Via Laterina 8, Siena 53100,
            Italy
FEATURES             Location/Qualifiers
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                     /note="rifampicin-resistant"
     gene            <1..>278
                     /gene="rpoB"
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                     /transl_table=11
                     /product="rifampicin-resistant RNA polymerase
                     beta-subunit"
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ORIGIN

  Query Match            [illegible];  Score [illegible];  DB 1;  Length 278;
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Qy          1 ACGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        [illegible] ACGGGTGCACGTCGCGGACCTCCA [illegible]

RESULT [illegible]
AF[illegible]
LOCUS       AF[illegible]               [illegible] bp    DNA     linear   BCT [illegible]-MAY-[illegible]
DEFINITION  Mycobacterium tuberculosis isolate [illegible] RNA polymerase beta subunit
            (rpoB) gene, partial cds.
ACCESSION   AF[illegible]
VERSION     AF[illegible].1  GI:[illegible]
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Orru,G., Tona,E., Viridomini,S., [illegible],M.R., Fatt[illegible]
            [illegible]
  TITLE     Intermediate Resistance to Rifampicin in Clinical [illegible]
            Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Orru,G. and Vi[illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-[illegible]) Dip. [illegible] Molecolare, [illegible]
            Microbiologia M[illegible]
            Viale Bracci, Siena 53100, Italy
FEATURES             Location/Qualifiers
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                     /organism="Mycobacterium tuberculosis"
                     /isolate="F[illegible]"
                     /db_xref="taxon:1773"
     gene            <1..>[illegible]
                     /gene="rpoB"
     CDS             <1..>[illegible]
                     /gene="rpoB"
                     /note="has intermediate resistance to 0.5 [illegible]
                     rifampicin"
                     /codon_start=1
                     /transl_table=11
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ORIGIN

  Query Match            [illegible];  Score [illegible];  DB 1;  Length [illegible];
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  Best Local Similarity [illegible] Pred. No. [illegible]
  Matches   24;  Conservative  [illegible]  Mismatches  [illegible]  Indels  [illegible]  Gaps  [illegible]

Qy          1 ACGGTGCACGTCGCGGACCTGCA 24
              ||||||||||||||||||||||
Db        [illegible] ACGGTGCACGTCGCGGACCTGCA [illegible]


RESULT 3
AF[illegible]
LOCUS       AF[illegible]    278 bp    DNA    linear   BCT 08-MAY-2001
DEFINITION  Mycobacterium tuberculosis isolate RM0[illegible] RNA polymerase beta subunit
            (rpoB) gene, partial cds.
ACCESSION   AF[illegible]
VERSION     AF[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 278)
  AUTHORS   [illegible] Lari,N., Vivi[illegible] [illegible],M.[illegible]
            [illegible] and [illegible]
  TITLE     Intermediate Resistance to Rifampicin in Clinical Isolates of
            Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 278)
  AUTHORS   [illegible] and Vivi[illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2001) Dip. Biologia Molecolare, Laboratorio di
            Microbiologia Molecolare e Biotecnologia, Universita' di Siena,
            Viale Bracci, Siena 53100, Italy
FEATURES             Location/Qualifiers
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                     /isolate="RM0[illegible]"
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BASE COUNT     [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 278;
  Best Local Similarity   [illegible];  Pred. No. [illegible]
  Matches   24;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible]

Qy          1 ACGGTGCACGTCGCGGACCTGCA 24
              ||||||||||||||||||||||
Db        [illegible] ACGGTGCACGTCGCGGACCTGCA [illegible]


RESULT 4
AF[illegible]
LOCUS       AF[illegible]    278 bp    DNA    linear   BCT 08-MAY-2001
DEFINITION  Mycobacterium tuberculosis isolate RM[illegible] RNA polymerase beta subunit
            (rpoB) gene, partial cds.
ACCESSION   AF[illegible]
VERSION     AF[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 278)
  AUTHORS   [illegible] Lari,N., Vivi[illegible] [illegible],M.[illegible]
            [illegible] and [illegible]
  TITLE     Intermediate Resistance to Rifampicin in Clinical Isolates of
            Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 278)
  AUTHORS   [illegible] and Vivi[illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2001) Dip. Biologia Molecolare, Laboratorio di
            Microbiologia Molecolare e Biotecnologia, Universita' di Siena,
            Viale Bracci, Siena [illegible], Italy
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                     LSPEPA[illegible]LEVRDVHPSHYGRM[illegible]IETPEGPNIG[illegible]VYARVNPF[illegible]"
BASE COUNT     [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible]
  Matches   24;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible]

Qy          1 ACGGTGCACGTCGCGGACCTGCA 24
              ||||||||||||||||||||||
Db        [illegible] ACGGTGCACGTCGCGGACCTGCA [illegible]


RESULT 5
AF[illegible]
LOCUS       AF[illegible]    [illegible] bp    DNA    [illegible]
DEFINITION  Mycobacterium [illegible] RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF[illegible]
VERSION     AF[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Mycobacterium [illegible]
  ORGANISM  Mycobacterium [illegible]
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium [illegible] complex.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., [illegible]
            Kim,[illegible], Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. [illegible] (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Kook,Y.H., Kim,B.J., [illegible] Lyu,M.A., Kim,[illegible]
            Kim,S.J., Cha,C.Y., Kim,[illegible] and [illegible],Y.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) [illegible], Seoul National University
            College of Medicine, [illegible]
            Korea
```

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FEATURES             Location/Qualifiers
     source          1..306
                     /organism "Mycobacterium africanum"
                     /strain "ATCC25420"
                     /db_xref "ATCC:25420"
                     /db_xref "taxon:33894"
     gene            <1..>306
                     /gene "rpoB"
     CDS             <1..>306
                     /gene "rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id "AAD55514.1"
                     /db_xref "GI:5902488"
                     /translation="[illegible]
                     VVAAIKEFFGTS[illegible]"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        254 AAGGGTGCACGTCGCGGACCTCCA 277

RESULT 7
AF057451/c
LOCUS       AF057451                 306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION   AF057451
VERSION     AF057451.1  GI:5902489
KEYWORDS    .
SOURCE      Mycobacterium bovis.
  ORGANISM  Mycobacterium bovis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1..306
                     /organism "Mycobacterium bovis"
                     /strain "ATCC19210"
                     /db_xref "ATCC:19210"
                     /db_xref "taxon:1765"
     gene            <1..>306
                     /gene="rpoB"
     CDS             <1..>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product "RNA polymerase beta"
                     /protein_id "AAD55515.1"
                     /db_xref "GI:5902490"
                     /translation "RIVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIR
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BASE COUNT       [illegible]
ORIGIN

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Qy          1 AAGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        306 AAGGGTGCACGTCGCGGACCTCCA 277

RESULT 8
AF057452/c
LOCUS       AF057452                 306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
            (rpoB) gene, partial cds.
ACCESSION   AF057452
VERSION     AF057452.1  GI:5902491
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1..306
                     /organism "Mycobacterium bovis BCG"
                     /strain "French 1173P2"
                     /db_xref "taxon:33892"
     gene            <1..>306
                     /gene "rpoB"
     CDS             <1..>306
                     /gene "rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product "RNA polymerase beta"
                     /protein_id "AAD55516.1"
                     /db_xref "GI:5902492"
                     /translation "RIVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIR
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BASE COUNT       [illegible]
ORIGIN

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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        300 AAGGGTGCACGTCGCGGACCTCCA 277

RESULT 9
AF057453/c
LOCUS       AF057453                 306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial
            cds.
```

```
ACCESSION   AF[illegible]
VERSION     AF[illegible]
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.C. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University,
            College of Medicine, 28 Yungun-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Mycobacterium bovis BCG"
                     /strain="Tokyo 172"
                     /db_xref="taxon:[illegible]"
     gene            [illegible]
                     /gene="rpoB"
     CDS             [illegible]
                     /gene="rpoB"
                     /codon_start=[illegible]
                     /transl_table=[illegible]
                     /product="RNA polymerase beta"
                     /protein_id="AAD[illegible]"
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                     /translation="[illegible]
                     VVAAIKE[illegible]"
BASE COUNT   [illegible]
ORIGIN

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Qy          [illegible] A[illegible]A[illegible]A 24
                 [illegible]
Db          [illegible] A[illegible]A[illegible]A [illegible]


RESULT [illegible]
AF[illegible]
LOCUS       AF[illegible]   [illegible] bp    DNA     linear   BCT [illegible]
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF[illegible]
VERSION     AF[illegible]
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.C. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University,
            College of Medicine, 28 Yungun-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
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                     /organism="Mycobacterium tuberculosis"
                     /strain="[illegible]"
                     /db_xref="ATCC:[illegible]"
                     /db_xref="taxon:[illegible]"
     gene            [illegible]
                     /gene="rpoB"
     CDS             [illegible]
                     /gene="rpoB"
                     /codon_start=[illegible]
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                 /transl_table=11
                 /product="RNA polymerase beta"
                 /protein_id="AAD55521.1"
                 /db_xref="GI:5902502"
                 /translation="RIVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIR
                 VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       50 a    109 c    101 g     46 t
ORIGIN

  Query Match            100.0%;  Score 24;  DB 1;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACGGCGCAGGCGCGGAGCGCGA 24
              ||||||||||||||||||||||||
Db        254 ACGGCGCAGGCGCGGAGCGCGA 277


RESULT 12
AF057466/c
LOCUS       AF057466               306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium gastri RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION   AF057466
VERSION     AF057466.1  GI:5902519
KEYWORDS    .
SOURCE      Mycobacterium gastri.
  ORGANISM  Mycobacterium gastri
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1..306
                     /organism="Mycobacterium gastri"
                     /strain="ATCC15754"
                     /db_xref="ATCC:15754"
                     /db_xref="taxon:1777"
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                     /gene="rpoB"
     CDS             <1..>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
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                     /translation="RIVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIR
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       52 a    102 c    103 g     49 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACGGCGCAGGCGCGGAGCGCGA 24
              ||||||||||||||||||||||||
Db        254 ACGGCGCAGGCGCGGAGCGCGA 277


RESULT 13
AF057479/c
LOCUS       AF057479               306 bp    DNA     linear   [illegible]
DEFINITION  Mycobacterium avium subsp. paratuberculosis RNA [illegible]
            (rpoB) gene, partial cds.
ACCESSION   AF057479
VERSION     AF057479.1  GI:[illegible]
KEYWORDS    .
SOURCE      Mycobacterium avium subsp. paratuberculosis.
  ORGANISM  Mycobacterium avium subsp. paratuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium avium complex (MAC).
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., [illegible]
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative [illegible]
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., [illegible]
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National [illegible]
            College of Medicine, 28 Yongon-dong, Chongno-gu, [illegible]
            Korea
FEATURES             Location/Qualifiers
     source          1..306
                     /organism="Mycobacterium avium subsp. paratuberculosis"
                     /strain="ATCC19698"
                     /sub_species="paratuberculosis"
                     /db_xref="ATCC:19698"
                     /db_xref="taxon:1770"
     gene            <1..>306
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     CDS             <1..>306
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                     /db_xref="GI:[illegible]"
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BASE COUNT       [illegible]
ORIGIN

  Query Match            [illegible];  Score 24;  DB 1;  Length 306;
  Best Local Similarity  [illegible];  Pred. No. [illegible];
  Matches   24;  Conservative    [illegible];  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy          1 ACGGCGCAGGCGCGGAGCGCGA 24
              ||||||||||||||||||||||||
Db        254 ACGGCGCAGGCGCGGAGCGCGA 277


RESULT 14
AR157003/c
LOCUS       AR157003               [illegible] bp    DNA     linear   [illegible]
DEFINITION  Sequence 2 from patent US [illegible]
ACCESSION   AR157003
VERSION     AR157003.1  GI:[illegible]
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Kook,Y.H. and Kim,B.J.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
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[illegible]

/ [illegible] "unknown"

[illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible]

DNA [illegible]

Method for identifying [illegible] species by comparative sequence analysis of [illegible]

/ [illegible] "unknown"

[illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible]

(without alignments)

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N Geneseq [illegible]*

SUMMARIES

Description

ALIGNMENTS

XX
XX
XX
PF Rifampin [illegible]
XX
KW Rifampin [illegible]
KW nested polymerase [illegible]
KW Single strand [illegible]
XX
OS Unidentified.
XX
XX
XX
XX
XX
PA (K[illegible]K/) K[illegible]K Y H
XX
PI Kook YH [illegible]
XX
DR WPI; [illegible]
XX
PT Method for detection of [illegible] Mycobacterium [illegible]
PT nested polymerase chain reaction [illegible]

```
[illegible]   [illegible] [illegible]ism (PCR SSCP) and single step nested PCR SSCP targeting RPOB
[illegible]   DNA [illegible] N Abstract
XX
[illegible]   [illegible] state; Fig 4; 23pp; Korean.
XX
[illegible]   The invention relates to a method for detection of rifampin tolerant
[illegible]   Mycobacterium tuberculosis by nested polymerase chain reaction-single
[illegible]   strand conformational polymorphism (PCR-SSCP) and single step nested
[illegible]   PCR SSCP targeting ROPB DNA. This sequence represents a rifampin tolerant
[illegible]   Mycobacterium tuberculosis identification method associated
[illegible]   [illegible]ide.
XX
[illegible]   Sequence 228 BP; 42 A; 78 C; 74 G; 34 T; 0 other;

  Query Match             100.0%;  Score 24;  DB 21;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. [illegible].27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

[illegible]          1 A[illegible]GA[illegible]GGACCTCCA 24
                       [illegible]
[illegible]        [illegible] A[illegible]GTGCAGGTCGCGGACCTCCA 197


RESULT [illegible]
AA[illegible]
[illegible]   AA[illegible] standard; DNA; [illegible] BP.
XX
AC   AA[illegible];
XX
[illegible]   [illegible] MAR [illegible] (first entry)
XX
[illegible]   Mycobacterium species identification primer #4.
XX
KW   Drug resistance detection; mycobacterial species identification; probe;
KW   oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW   primer.
XX
OS   Mycobacterium avium.
XX
PN   W[illegible] [illegible]573 A1.
XX
[illegible]   [illegible] [illegible] 2001.
XX
[illegible]   [illegible] MAY-2001; 2001WO-KR00904.
XX
[illegible]   [illegible] MAY-2[illegible]; 2000KR-0029369.
XX
PA   ([illegible]) [illegible] MEDIAB CO LTD.
XX
[illegible]   Kim H, Kim N, Y[illegible] S, Kim J, Park M;
XX
[illegible]   W[illegible] [illegible]75472/10.
XX
[illegible]   Kit for mycobacterial species identification and drug resistance
[illegible]   detection, has oligonucleotide chip with species identification probe,
[illegible]   mycobacterial drug resistance detection probe, and its contrast group
[illegible]   probe.
XX
[illegible]   [illegible] state; Page 21; 74pp; English.
XX
[illegible]   The invention relates to a diagnostic kit for mycobacterial species
[illegible]   identification and drug resistance detection comprising an
[illegible]   oligonucleotide chip including a species identification probe, a
[illegible]   mycobacterial drug-resistance detection probe, a contrast group probe
[illegible]   corresponding to each drug resistance detection probe, and a marker for
[illegible]   detecting a hybridisation of the oligonucleotide chip and a specimen. The
[illegible]   identification probe is comprised of species-specific DNA sequences of
[illegible]   mycobacterial rpoB gene and the detection probe is comprised of one or
[illegible]   [illegible] modified codons of mycobacterial rpoB gene. The method involves
[illegible]   amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
[illegible]   (PCR) and discriminating species by fluorescent intensity corresponding
[illegible]   to a particular species. The specimen is preferably uncultured sputum,
[illegible]   [illegible] or cerebrospinal fluid of a patient. Sequences AAS[illegible]478 AAS[illegible]
[illegible]   represent mycobacterial species identification probes and [illegible] the
[illegible]   invention.
XX
SQ   Sequence 300 BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score 2[illegible];  DB 24;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   24;  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy          1 A[illegible]A 24
                [illegible]
Db        [illegible] A[illegible]A [illegible]


RESULT 3
AAX27214
ID   AAX27214 standard; DNA; [illegible] BP.
XX
AC   AAX27214;
XX
DT   27 MAY [illegible] (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; [illegible]
XX
OS   Mycobacteria tuberc[illegible].
XX
PN   W[illegible] A[illegible].
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998; [illegible]KR-[illegible].
XX
PR   28-JUL-1997; 97KR-[illegible].
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B, Kook Y;
XX
DR   WPI; 1998-[illegible]/1[illegible].
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence specific amplification of the rpoB gene from my[illegible]
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 4; Page [illegible]; [illegible]pp; English.
XX
CC   This sequence represents a [illegible]bacterial rpoB gene fragment that is
CC   amplified using the PCR primers of the invention. The primers [illegible]
CC   method of detecting and identifying mycobacterial species [illegible]
CC   a phylogenetic tree for the species. The use of the primers [illegible]
CC   sequence specific amplification of the rpoB gene (encoding [illegible]
CC   subunit of RNA polymerase) from mycobacterial species [illegible]
CC   efficient way of characterising these species. In addition [illegible]
CC   phylogenetic analysis, the rpoB gene can be used as an [illegible]
CC   the 16S rRNA gene because it has four subunits, which are [illegible]
CC   conserved throughout prokaryotes. The method is particularly [illegible]
CC   slow growing, fastidious or unidentifiable mycobacteria. An[illegible]
CC   susceptibility can be simultaneously determined in M. tuber[illegible]
XX
SQ   Sequence 306 BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score 2[illegible];  DB 19;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   24;  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy          1 A[illegible]A 24
                [illegible]
Db        [illegible] A[illegible]A [illegible]
```

```
[illegible]
AAX[illegible]
ID   AAX[illegible] standard; DNA; [illegible] BP.
XX
AC   AAX[illegible]
XX
DT   [illegible] MAY [illegible] (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis.
XX
OS   Mycobacterium [illegible]
XX
PN   WO[illegible]-A1.
XX
PD   [illegible]-FEB-[illegible].
XX
PF   [illegible]-JUL-[illegible]; [illegible]KR-[illegible].
XX
PR   [illegible]; [illegible]KR-[illegible].
XX
PA   ([illegible]) [illegible] NEHR [illegible]
XX
PI   Kim B, Kook Y;
XX
DR   WPI; [illegible]/16.
XX
PT   New pair of polymerase chain reaction (PCR) primers [illegible] for
PT   sequence specific amplification of the rpoB gene from mycobacteria,
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim [illegible]; Page [illegible]; [illegible]pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match              [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity    [illegible]%;  Pred. No. [illegible];
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    [illegible];

Qy          1 A[illegible]A 24
              [illegible]
Db          [illegible] A[illegible]A [illegible]


RESULT [illegible]
AAX[illegible]
ID   AAX[illegible] standard; DNA; [illegible] BP.
XX
AC   AAX[illegible]
XX
DT   [illegible] MAY [illegible] (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis.
XX
OS   Mycobacterium africanum.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible]-FEB-[illegible].
XX
PF   [illegible]-JUL-[illegible]; [illegible]KR-[illegible].
XX
PR   [illegible]; [illegible]KR-[illegible].
XX
PA   ([illegible]) [illegible] NEHR [illegible]
XX
PI   Kim B, Kook Y;
XX
DR   WPI; [illegible].
XX
PT   New pair of polymerase chain reaction (PCR) primers [illegible]
PT   sequence specific amplification of the rpoB gene from mycobacteria,
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match              [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity    [illegible]%;  Pred. No. [illegible];
  Matches   24;  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy          1 A[illegible]A 24
              [illegible]
Db          [illegible] A[illegible]A [illegible]


RESULT [illegible]
AAX[illegible]
ID   AAX[illegible] standard; DNA; [illegible] BP.
XX
AC   AAX[illegible]
XX
DT   [illegible] MAY [illegible] (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis.
XX
OS   Mycobacterium [illegible]
XX
PN   WO[illegible]-A1.
XX
PD   [illegible]-FEB-[illegible].
XX
PF   [illegible]-JUL-[illegible]; [illegible]KR-[illegible].
XX
PR   [illegible]; [illegible]KR-[illegible].
XX
PA   ([illegible]) [illegible] NEHR [illegible]
XX
PI   Kim B, Kook Y;
XX
DR   WPI; [illegible].
```

```
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 7; Page 63-64; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis
XX
SQ   Sequence 306 BP; 50 A; 109 C; 101 G; 46 T; 0 other;

  Query Match             100.0%;  Score 24;  DB 19;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        254 ACGGGTGCACGTCGCGGACCTCCA 277


RESULT 7
AAX27[illegible]
ID   AAX27[illegible] standard; DNA; 306 BP.
XX
AC   AAX27[illegible];
XX
DT   27 MAY 1999  (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; ss.
XX
OS   Mycobacteria bovis.
XX
FN   Wo[illegible]Al.
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998;   98KR-0030228.
XX
PR   28-JUL-1997;   97KR-0035501.
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B,  Kook Y;
XX
DR   WPI; 1999-[illegible]67/46.
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 9; Page 64; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis
XX
SQ   Sequence 306 BP; [illegible] A; [illegible] C; [illegible] G; 47 T; 0 other;

  Query Match             100.0%;  Score 24;  DB 19;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        306 ACGGGTGCACGTCGCGGACCTCCA 2[illegible]


RESULT 8
AAX27[illegible]
ID   AAX27[illegible] standard; DNA; [illegible] BP.
XX
AC   AAX27[illegible];
XX
DT   27 MAY 1999  (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; [illegible]
XX
OS   Mycobacteria bovis
XX
FN   Wo[illegible]Al.
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998;   98KR-[illegible]
XX
PR   28-JUL-1997;   97KR-[illegible]
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B,  Kook Y;
XX
DR   WPI; 1999-[illegible]67/46.
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 9; Page 64; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; 47 T; 0 other;

  Query Match             100.0%;  Score 24;  DB 19;  Length [illegible];
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACGGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
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```
                ATTTTTTATTTTTTTATTTTA 27

[illegible]
AA[illegible]
     AA[illegible] standard; DNA; [illegible] BP.
XX
     AA[illegible]
XX
     [illegible] MAR [illegible] (first entry)
XX
     rpoB gene fragment.
XX
KW   rpoB gene; mycobacterial phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; ss.
XX
     Mycobacterium [illegible]
XX
     W[illegible]
XX
     [illegible]
XX
     [illegible] KR [illegible]
XX
     [illegible] KR [illegible]
XX
PA   [illegible] NEEK [illegible]
XX
     [illegible] K Y
XX
     [illegible]/[illegible]
XX
     New pair of polymerase chain reaction (PCR) primers - for
     sequence specific amplification of the rpoB gene from mycobacterial
     species, useful for detecting and identifying mycobacterial species
XX
     [illegible] English.
XX
     This sequence represents a mycobacterial rpoB gene fragment, that is
     amplified using the PCR primers of the invention. The primers form a
     method of detecting and identifying mycobacterial species by constructing
     a phylogenetic tree for the species. The use of the primers for
     sequence specific amplification of the rpoB gene (encoding the beta
     subunit of RNA polymerase) from mycobacterial species provides an
     efficient way of characterising these species. In addition to
     phylogenetic analysis, the rpoB gene can be used as an alternative to
     the 16S rRNA gene because it has four subunits, which are highly
     conserved throughout prokaryotes. The method is particularly useful for
     [illegible] identification of uncultivatable mycobacteria. Also, rifampicin
     susceptibility can be simultaneously determined in M. tuberculosis.
XX
     Sequence [illegible] BP; [illegible] A; [illegible] other;

  Query Match             [illegible] Score [illegible] DB [illegible] Length [illegible]
  Best Local Similarity   [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

                ATTTTTTATTTTTTTATTTTA 24
                |||||||||||||||||||||
                ATTTTTTATTTTTTTATTTTA 27

[illegible]
AA[illegible]
     AA[illegible] standard; DNA; [illegible] BP.
XX
AC   AA[illegible]
XX
     [illegible] MAR [illegible] (first entry)
XX
     M[illegible] bacterial [illegible] species identification primer #1.
XX
KW   [illegible] resistance detection; mycobacterial species identification probe;
KW   [illegible] [illegible] [illegible]
KW   primer.
XX
OS   Mycobacterium [illegible]
XX
PN   W[illegible]-A.
XX
PD   [illegible]-DEC-2001.
XX
PF   [illegible]-MAY-2001; [illegible] KR [illegible]
XX
PR   [illegible]-MAY-2[illegible] KR [illegible]
XX
PA   (BIOM-) BIOMEDLAB [illegible]
XX
PI   Kim B, Kim N, Y[illegible], K[illegible], [illegible] M
XX
DR   WPI; 2002-[illegible]/[illegible]
XX
PT   Kit for mycobacterial species identification and drug resistance
PT   detection, has [illegible] species identification probe
PT   a mycobacterial drug resistance detection probe [illegible]
PT   probe
XX
PS   Disclosure; Page [illegible]; [illegible] English.
XX
CC   The invention relates to [illegible] mycobacterial species
CC   identification and drug resistance detection [illegible]
CC   oligonucleotide chip containing a species identification probe [illegible]
CC   mycobacterial drug resistance detection probe [illegible]
CC   corresponding to each drug resistance detection probe [illegible]
CC   detecting a hybridisation of the oligonucleotide chip and [illegible]
CC   identification probe [illegible] species. DNA [illegible]
CC   mycobacterial rpoB gene and the detection probe is [illegible]
CC   more modified codons [illegible] rpoB gene. The method [illegible]
CC   amplifying rpoB gene fragments [illegible] by polymerase chain reaction
CC   (PCR) and discriminating species by the relevant intensity [illegible]
CC   to a particular species. The specimen is preferably [illegible]
CC   blood or cerebrospinal fluid of a patient. Sequences AA[illegible]
CC   represent mycobacterium species identification probes and [illegible]
CC   invention.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] other;

  Query Match             [illegible] DB [illegible] Length [illegible]
  Best Local Similarity   [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy              ATTTTTTATTTTTTTATTTTA 24
                |||||||||||||||
Db           [illegible] ATTTTTTATTTTTTTATTTTA [illegible]

RESULT [illegible]
AA[illegible]
ID   AA[illegible] standard; DNA; [illegible]
XX
AC   AA[illegible]
XX
DT   12-MAR-2002 (first entry)
XX
DE   Mycobacterium species [illegible] #.
XX
KW   Drug resistance detection; mycobacterial species identification probe;
KW   oligonucleotide chip; [illegible]
KW   primer.
XX
OS   Mycobacterium [illegible]
XX
PN   W[illegible]-A.
XX
PD   [illegible]-DEC-2001.
XX
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```
PF   30-MAY-2001; 2001WO-KR00904.
XX
PR   30-MAY-2000; 2000KR-0029369.
XX
PA   (BIOM-) BIOMEDLAB CO LTD.
XX
PI   Kim H,  Kim N,  Yoon S,  Kim J,  Park M;
XX
DR   WPI; 2002-[illegible]472/10.
XX
PT   Kit for mycobacterial species identification and drug resistance
PT   detection, has oligonucleotide chip with species identification probe,
PT   a mycobacterial drug-resistance detection probe, and its contrast group
PT   probe -
XX
PS   Disclosure; Page 21; 74pp; English.
XX
CC   The invention relates to a diagnostic kit for mycobacterial species
CC   identification and drug resistance detection comprising an
CC   oligonucleotide chip including a species identification probe, a
CC   mycobacterial drug resistance detection probe, a contrast group probe
CC   corresponding to each drug resistance detection probe, and a marker for
CC   detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC   identification probe is comprised of species-specific DNA sequences of
CC   mycobacterial rpoB gene and the detection probe is comprised of one or
CC   more modified codons of mycobacterial rpoB gene. The method involves
CC   amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC   (PCR) and discriminating species by fluorescent intensity corresponding
CC   to a particular species. The specimen is preferably uncultured sputum,
CC   blood or cerebrospinal fluid of a patient. Sequences AAS9[illegible]478-AAS9[illegible]
CC   represent mycobacterium species identification probes and primers of the
CC   invention.
XX
SQ   Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

  Query Match             100.0%;  Score 24;  DB 24;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 A[illegible]GACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        254 AA[illegible]GGTGCACGTCGCGGACCTCCA 277


RESULT 12
AAS9[illegible]
ID   AAS9[illegible] standard; DNA; 306 BP.
XX
AC   AAS9[illegible];
XX
DT   12-MAR-2002  (first entry)
XX
DE   Mycobacterium species identification primer #5.
XX
KW   Drug resistance detection; mycobacterial species identification; probe;
KW   oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW   primer.
XX
OS   Mycobacterium bovis.
XX
PN   WO200192[illegible]-A1.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-KR00904.
XX
PR   30-MAY-2000; 2000KR-0029369.
XX
PA   (BIOM-) BIOMEDLAB CO LTD.
XX
PI   Kim H,  Kim N,  Yoon S,  Kim J,  Park M;
XX
DR   WPI; 2002-[illegible]472/10.
XX
PT   Kit for mycobacterial species identification and drug resistance
PT   detection, has oligonucleotide chip with species identification probe,
PT   a mycobacterial drug resistance detection probe, and its contrast group
PT   probe -
XX
PS   Disclosure; Page 21; 74pp; English.
XX
CC   The invention relates to a diagnostic kit for mycobacterial species
CC   identification and drug resistance detection comprising an
CC   oligonucleotide chip including a species identification probe, a
CC   mycobacterial drug resistance detection probe, a contrast group probe
CC   corresponding to each drug resistance detection probe, and a marker for
CC   detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC   identification probe is comprised of species specific DNA sequences of
CC   mycobacterial rpoB gene and the detection probe is comprised of one or
CC   more modified codons of mycobacterial rpoB gene. The method involves
CC   amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC   (PCR) and discriminating species by fluorescent intensity corresponding
CC   to a particular species. The specimen is preferably uncultured sputum,
CC   blood or cerebrospinal fluid of a patient. Sequences AAS9[illegible]478-AAS9[illegible]
CC   represent mycobacterium species identification probes and primers of the
CC   invention.
XX
SQ   Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

  Query Match             [illegible];  Score 24;  DB 24;  Length 306;
  Best Local Similarity   [illegible];  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGGTGCACGTCGCGGACCTCCA 24
              ||||||||||||||||||||||||
Db        306 AACGGTGCACGTCGCGGACCTCCA 2[illegible]


RESULT 13
AAS9[illegible]
ID   AAS9[illegible] standard; DNA; [illegible] BP.
XX
AC   AAS9[illegible];
XX
DT   12-MAR-2002  (first entry)
XX
DE   Mycobacterium species identification primer #6.
XX
KW   Drug resistance detection; mycobacterial species identification; probe;
KW   oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW   primer.
XX
OS   Mycobacterium bovis.
XX
PN   WO200192[illegible]-A1.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-KR00904.
XX
PR   30-MAY-2000; 2000KR-0029369.
XX
PA   (BIOM-) BIOMEDLAB CO LTD.
XX
PI   Kim H,  Kim N,  Yoon S,  Kim J,  Park M;
XX
DR   WPI; 2002-[illegible]472/10.
XX
PT   Kit for mycobacterial species identification and drug resistance
PT   detection, has oligonucleotide chip with species identification probe,
PT   a mycobacterial drug resistance detection probe, and its contrast group
PT   probe -
XX
PS   Disclosure; Page 21; 74pp; English.
XX
CC   The invention relates to a diagnostic kit for mycobacterial species
```

[illegible]

CC (PCR) and discriminating species by fluorescent intensity [illegible]
CC [illegible] particular species. The specimen is preferably [illegible]
CC blood or cerebrospinal fluid of a patient. Sequences [illegible]
CC represent mycobacterial species identification probes and primers [illegible]
CC invention.
XX
SQ Sequence [illegible]

Query Match [illegible]
Best Local Similarity [illegible] Pred. No. [illegible]
Matches [illegible] Mismatches [illegible]

Qy [illegible]

Db [illegible]

RESULT [illegible]
AAS[illegible]
ID AAS[illegible] standard; DNA; [illegible]
XX
AC AAS[illegible]
XX
DT [illegible] MAR [illegible] (first entry)
XX
DE Mycobacterium species identification primer [illegible]
XX
KW Drug resistance detection; mycobacterial species identification [illegible]
KW [illegible]
KW primer.
XX
OS Mycobacterium [illegible]
XX
PN W[illegible]
XX
PD [illegible]
XX
PF [illegible] MAY [illegible]
XX
PR [illegible] MAY [illegible]
XX
PA (BIOM-) BIOMEDLAB [illegible]
XX
PI Kim H, Kim N, [illegible]
XX
DR WPI; [illegible]
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has diagnostic [illegible] chip with species identification probe,
PT mycobacterial drug resistance detection probes, [illegible]
PT probe
XX
PS Disclosure; [illegible]
XX
CC The invention relates to [illegible]
CC identification and drug resistance detection comprising [illegible]
CC oligonucleotide chip [illegible]
CC mycobacterial drug resistance detection probes [illegible]
CC corresponding [illegible]
CC detecting a hybridization [illegible]
CC identification probe [illegible]
CC mycobacterial rpoB gene and the detection probe [illegible]
CC more modified [illegible]
CC amplifying [illegible]
CC (PCR) and discriminating species by fluorescent intensity [illegible]
CC [illegible] particular species. [illegible]
CC blood or cerebrospinal fluid of a patient. Sequences [illegible]
CC represent mycobacterial species identification probes [illegible]
CC invention.
XX
SQ Sequence [illegible]

Query Match [illegible]

[illegible]

```
  [illegible] Similarity [illegible]; Pred. No. [illegible];
  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 A[illegible]ACGTCGGGACCTCCA 24
                [illegible]
Db          [illegible] A[illegible]GCACGTCGGGACCTCCA 277

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